Command line parameters:
  -MODEL-frame-p2n.model   DEV.xlp
  -Q=.gn2_1/USP2/gcqdata/qcgseq/geneseq/genesep/NA2000_[3374]_21/pff-query.fasta_1_2Ht
  -DB-N_Geneseq_1101 -QFMF-fastap -SUFFIX-rng -GAPOP-12.000
  -GAPEXT-4.000 -MINMATCH-0.100 -LOWPEXT-0.000 -LOWPEXT=0.000
  -QGAPOP-4.500 -QGAPEXT=0.050 -XGAPOP-10.000 -XGAPEXT=0.500
  -FGAPOP-6.000 -FGAPEXT=7.000 -YGAPOP-10.000 -YGAPEXT=0.500
  -DELOP-6.000 -DELEXT-7.000 -START-1 -MATRIX-blosum62
  -TRANS-human40.cdi -LIST-45 -DECAL-ON=200 -THR_SCORF-pct
  -NOPM-ex' -MINLEN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pfs
  -USEP-US09525998_3CGN1_1_257 NCPU-6 ICPU-3 LONGLOG NO_XLFXY
  -WAIT -THREADS-1

Search information block:
  Query: US-09-525-998A.12
  Query length: 200
  Database: N_Geneseq_1101:*
  Database sequences: 930621
  Database length: 428662619
  Search time (sec): 247.030000

score_list:
Sequence   Strd Orig   ZScore   EScore len Documentation

seq_name: ...

seq_documentation_block:
  ID AAQ64292 standard; DNA, 1341 nr.
  XX
  AC AAQ64292;
  XX
  DT 29-JAN-1991 (first entry)
  XX
  DE Plasmid Tumour Necrosis Factor Binding Protein 15 cDNA insert.
  XX
  KW Tumour necrosis factor binding protein; TNF BP; TNF receptor;
  KW TNF BP15; BS.
  XX
  OS Homo sapiens.
  XX
  FH Key   Location/Qualities
  FT CDS   213..1325
  FT   /*tag=..a
  FT   /product=TNF BP
  XX
  PN EP393438-A.
  XX
  PD 24-OCT-1990.
  XX
  PF 06-APR-1990; 9CEP-0106624.

  DNA encoding TNF binding protein and TNF receptor used in
  tumour treatment and to understand mechanism to TNF action

  Disclosed by: ...

alignment_scores:
  Quality: 1117.50   Length: ...
  Ratio: ...
  Percent Similarity: 94.203   Percent Identity: 94.203

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XX
FH    Key                Location/Qualifiers
FT    CDS                1..1366
FT                       /*tag- a
FT                       /product= hTNF-R
FT    sig_peptide        1..120
FT                       /*tag- b
FT    mat_peptide        121..1363
FT                       /*tag- c
XX
PN    WO9319777-A.
XX
PD    14-OCT-1993.
XX
PF    26-MAR-1993;  93WO-US02938.
XX
PR    30-MAR-1992;  92US-0860710.
XX
PA    (IMMV ) IMMUNEX CORP.
XX
PI    Smith CA;
XX
DR    WPI: 1993-336592/42.
DR    P-PSDB; AAR42059.
XX
FT    New fusion protein tumour necrosis factor and human interleukin-1
PT    receptor - useful in therapy, diagnosis and assays of e.g.
PT    rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
XX
PS    Disclosure, Page 57-59, 85pp; English.
XX
CC    The sequences given in AAQ49931-32 encode human tumour necrosis factor
CC    receptor (TNF-R) and the sequences in AAQ49933-34 encode human
CC    interleukin-1 receptor (IL-1R).  These sequences were used in the
CC    production of a fusion protein which conformed to one of the
CC    formulae:
CC         TNF-R-linker-TNF-R-linker-IL-1R
CC         IL-1R-linker TNF R linker-TNF-R or
CC         TNF-R-linker-TNF-R
CC    The linker may comprise 4-100 amino acids selected from Gly, Asp,
CC    Ser, Thr and Ala.  These linkers separate the individual moieties
CC    by such a distance that each component of the fusion protein is
CC    capable of folding into the secondary or tertiary structure required
CC    for its biological activity.  These fusion proteins may be used in
CC    therapy, diagnosis and assays for conditions mediated by TNF or IL-1,
CC    particularly in conditions in which both TNF and IL-1 play a causitive
CC    role.  They may be used to treat cachexia, rheumatoid arthritis,
CC    diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,
CC    cerebral malaria, allograft and xenograft rejection in graft verses
CC    host disease, sepsis, septic shock, inflammation, allergies and
CC    autoimmune dysfunctions.
XX
SQ    Sequence 1368 BP; 292 A; 424 C; 376 G; 276 T; 0 other;
```

```
alignment_scores:
          Quality:  1117.50          Length:       211
          Ratio:    5.588            Gaps:           1
Percent Similarity:  94.787    Percent Identity:  94.787

alignment_block:
US-09-525-998A-12 x AAQ49932

Align seq 1/1   to: AAQ49932   from: 1  to: 1168

    1 MetGlyLeuSerThrValProAspLeuLeuProLeuValLeuonLeuGl 17
      |||||||||||||||||||||||||||||||||||||||||||||||||
    1 ATGGGCCTCTCCACCGTCCA...
```

```
    1 MetGlyLeuSerThrValProAspLeuLeuProLeuValLeuonLeuGl 17
      |||||||||||||||||||||||||||||||||||||||||||||||||
  212 ATGGGCCTCTCCACCGTCCA...

   17 uLeuLeuValGlyIleTyrProSerGlyValIleGly............... 29
      ||||||||||||||||||||||||
  262 ...

   30 ...........AspSerValCysProGlnGlyLysTyrIle 39
      |||||||||||||||||||||||||
  313 TAGGGGACAGGGAGAGAACAAGAGATAGTGTGTGCCCAAGGAAAAATATC 362

   40 HisProGlnAsnAsnSerIleCysCysThrLysCysHisLysGlyThrTy 56
      |||||||||||||||||||||||||||||||||
  363 CACCCTCAAAATAATTGGATTTGCTGTACCAAGTGCCACAAAGGAACCTA 412

   56 rLeuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArgGluC 73
      |||||||||||||||||||||||||
  413 CTTGTACAATGACTGTCCAGGGCCAGGGCAGGATACCGACTGCAGGGAGT 462

   73 ysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 89
      ||||||||||||||||||
  463 CTGAGAGCGGGAGCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 512

   90 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCy 106
      ||||||||||||||||||||
  513 AGTTGCTCCAAATGCCAAAGGGAAATGGTTAGGTCAAGTAGAAATCTCTG 562

  106 sThrValAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgH 123
      |||||||||||||||||||||||||
  563 CACAGTGGACCGGGATACCGTGTGCGGCTGCAGGAAGAACCAGTACAGGC 612

  123 isTrpTrpSerGluAsnLeuPheGluCysPheAsnCysSerLeuCysLeu 139
      |||||||||||||||||||||||||
  613 ATTGGTGGAGTGAAAACTTGTTTGAATGCTTCAATTGCAGCCTCTGCCTC 662

  140 AsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCysTh 156
      ||||||||||||||||||||
  663 AATGGAACCGTACACCTCTGCTGTCAAGAGAAAACAGAACACTGTGTGCA 712

  156 rCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerA 173
      |||||||||||||||||||||
  713 CTTGCCATGCAGGCTTCTTCCTAAGAGAAAACGAGTGTGTCTCCTGTAGTA 762

  173 snCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 189
      |||||||||||||||||||||||||
  763 ACTGCAAGAAATCCTTGGAGTGCACCAAGCTGTGCCTACCCCAGATTGAG 812

  190 AsnValLysGlyThrGluAspSerGlyThrThr 200
      ||||||||||||||||||||
  813 AATGTTAAGGGCACTGAGGACTCAGGCACCACA 845
```

```
seq_name: /SEQSZ/gcgdata/geneseq/geneseqp/NA1993.DAT:AAQ49932
seq_documentation_block:
ID    AAQ49932 standard; cDNA to mRNA; 1368 BP.
XX
AC    AAQ49932;
XX
DT    29-APR-1994  (first entry)
XX
DE    Lambda-derived TNF-R cDNA.
XX
KW    Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
KW    IL-1R; fusion protein, linker, TNF, IL 1; cachexia, cerebral malaria,
KW    rheumatoid arthritis; diabetes, multiple sclerosis, septic shock,
KW    pulmonary fibrosis, silicosis, allograft, xenograft, rejection,
KW    graft verses host disease; sepsis; inflammation; allergy;
KW    autoimmune dysfunction; ss.
XX
OS    Homo sapiens.
OS    Lambda-gt10-7-ctnfbp.
```

```
   17 uLeuLeuValGlyIleTyrProSerGlyValIleGly............... 29
      ||||||||||||||||||||||||
   51 GCTCTTGGTGGGAATAATACCCTGCAGGGTTATTGGAGTGGTGGGCCACC 100
```

```
30   ..........AspSerValCysProGlnGlyTyrHis  39
101  TAGGGATAGGAGAAGAGAGAATAGTGTGTCCCTGGTCGGTGGTGCAAGAAAATATC  150
         ||||||||||||||||||||||||||||||||||||
40   HisProGlnAsnAspArgIleCysTyrGlyTyrGlnSerGlyThrTy  55
151  CACCCTCAAAATAATTCGATTTGCTGTACCAAGTGGCCACAAAGGAACCTA  200
         ||||||||||||||||||||||||||||||||||||
56   rLeuTyrAsnAspArgProGlyProGlyLeuAspPheThrAspCysArgGluC  73
201  CTTTATAATGATCGTCCAGGTCCAGGATAGGATTGACTGTAGGGAGT  250
         ||||||||||||||||||||||||||||||||||||
73   ysGluGlySerGlyProHisArgAspSerGluAspHisLeuArgHisCysIle  89
251  GTGAAGGAAGTTCTTCAGGTCCACACTGTACAAAACGGAAGTTCTC  300
         ||||||||||||||||||||||||||||||||||||
90   SerCysSerLysCysArgLysGlyMetGlyGlnValGlyIleGluSerSerCy  106
301  AGCTGCTCCAAATGCCCAAAGGAAATGGGTCAGGTGGAGAGATCTCTTCTTG  350
         ||||||||||||||||||||||||||||||||||||
106  sThrValAspArgAspThrValCysArgLysLysAsnGlnTyrArgH  123
351  CAACAGTGGACCGGGATACGGTGTGTAGAAAGAAACAATACGGC  400
         ||||||||||||||||||||||||||||||||||||
123  isTyrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu  139
401  ATTATTGGAGTGAAAACTTTTCAGTGCTTCAATTGCAGTCTGTGTC  450
         ||||||||||||||||||||||||||||||||||||
140  AsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCysTh  156
451  AATGGGACGGTGCACCTCTCCTGCCAAGAAAAGCAAAACACGGTGTGCAC  500
         ||||||||||||||||||||||||||||||||||||
156  rCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerA  173
501  CTGCCATGCAGGTTTTTTCTTAGAGAAAAATGAGTGTGTCTCTTGTAGCA  550
         ||||||||||||||||||||||||||||||||||||
173  snCysSer...GlnPro...SerGlnHisCys  189
551  ACTGTAGCAAAGGCCTGAGTGAAGTTGTGTACCCAGATTGAG  600
         ||||||||||||||||||||||||||||||||||||
190  AsnValLysGlyThrThrGluAspThrSerGlyThrThr  200
601  AATGTTAAGGGCACTGAGGACTCAGGCACCACA  633
```

seq_name: ...

seq_documentation_block:
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ID   AAA95105 standard; DNA; 1368 BP.
XX
AC   AAA95105;
XX
DT   12-JAN-2001 (first entry)
XX
DE   Human TNFR1 coding sequence.
XX
KW   TNFR1; tumour necrosis factor receptor polymorphism; human;
KW   tumour; cancer; apoptosis; bacterial infection; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1368
FT                   /tag- a
FT                   /product- "TNFR1"
FT   exon            1..39
FT                   /tag- b
FT                   /number- 1
FT   variation       replace(36,G)
FT                   /tag- c
FT   exon            40..193
FT                   /tag- d
FT                   /number- 2
FT   exon            194..322
FT                   /tag- e
FT   variation       replace(224,T)
FT                   /tag- f
FT   variation       replace(263,T)
FT                   /tag- q
FT   exon            324..472
FT                   /tag- h
FT                   /number- 4
FT   variation       replace(362,A)
FT                   /tag- i
FT   variation       replace(403,C)
FT                   /tag- j
FT   exon            474..551
FT                   /tag- k
FT                   /number- 5
FT   exon            552..625
FT                   /tag- l
FT                   /number- 6
FT   exon            626..739
FT                   /tag- m
FT                   /number- 7
FT   exon            740..768
FT                   /tag- n
FT                   /number- 8
FT   exon            744..1057
FT                   /tag- o
FT                   /number- 9
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FT                   /tag- p
FT                   /number- 10
XX
PN   WO200050436-A1.
XX
PD   31-AUG-2000.
XX
PF   ........... JS04606.
XX
PP   23-FEB-1999; 6009-0121514.
XX
PA   (GENA-) GENAISSANCE PHARM INC.
PA   (NAND/) NANDABALAN K.
PA   (SCHU/) SCHULZ V P.
PA   (STEP/) STEPHENS J C.
PA   (CHEW) CHEW A.
XX
PI   Nandabalan K, Schulz VP, Stephens JC, Chew A;
XX
DR   WPI; 2000-539052/49.
DR   P-PSDB; AAH23446.
XX
CC   The present invention relates to polymorphic variants of the tumour
CC   necrosis factor receptor 1 (TNFR1) gene, the present sequence is
CC   the coding sequence of the TNFR1 gene. The sequence of the whole gene is
CC   given in AAA95104, AAA95103 and AAA95104. The polymorphisms were
CC   identified by amplifying and sequencing regions of the gene. Twelve
CC   polymorphic loci were discovered in these twelve polymorphisms, four can
CC   cause a change in the TNFR1 protein. The TNFR1 polymorphisms may be
CC   useful for studying the biological function of TNFR1 as well as for
CC   identifying drugs targeting the protein for treatment of disorders
CC   related to its abnormal expression or function such as tumours,
CC   apoptosis related disorders and bacterial infection.
XX
SQ   Sequence 1368 BP; 292 A; 424 C; 378 G; 274 T; 0 other;
```

The present invention relates to polymorphic variants of a reference sequence
for tumour necrosis factor receptor 1 (TNFR1), useful for studying the
biological function of TNFR1 and identifying drugs targeting the
protein for treating disorders -

Claim 7; Fig 4; 79pp; English.

alignment_scores:
Quality: 1117.50   Length: 211
Ratio: 5.588   Gaps: 1
Percent Similarity: 94.787   Percent Identity: 94.787

alignment_block:
US-09-525-998A-12 x AAA95105

Align seq 1/1 to: AAA95105   from: 1 to: 1368

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   1 ATGGGCTTGTCCACTGTCCCTGAT...GTTGTGGTCCCTGGA  50

  17 uLeuLeuValGlyIleThrP:oScrGlyValIleGly.......  29
     |||||||||||||||||||||||||||||||||
  51 GCTGTTGCTGGGAATAACCCCGGGTTGCAGGCCCCTACC  100

  30 ...........AspSerValCysProGlnGlyLysTyrIle  39
     |||||||||||||||||||||||||||||
 101 TAGGGACAGGGAGAAGAGAATAGTCCCAAGGAAAATAATG  150

  40 HisProGlnAsnAsnSerIleCysCysThrLysCysGlyThrTy  56
     ||||||||||||||||||||||||||||||||||||||
 151 CACCCTCAAAATAATTCGATTTGTTGTACGAAGTGAGGAACCTA  200

  56 rLeuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArgGluC  73
     |||||||||||||||||||||||||||||||||||||||||
 201 CTTGTACAACGACTGTCCAGGCCCGGGCAGGATACGGACTGCAGGGAGT  250

  73 ysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu  89
     |||||||||||||||||||||||||||||||||||||
 251 GTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACATGCCTC  300

  90 SerCysSerCysArgGlyLysGluMetGlyValGluValGlu..SerSerCy 106
     |||||||||||||||||||||||||||||||||||||||||||
 301 AGTTGCTCCTCAAATGCCAAAGGGAAATGGGTCAGTGGAGAT TCTTCTTG  350

 106 sThrValAspArgAspAspThrValCysGlyCysArgLysAsnGlnTyrArgH 123
     |||||||||||||||||||||||||||||||||||||||||
 351 CACAGTGGACCGGGACTACAGTCTGGG AGGAAGAAACAGTACCGGC  400

 123 isTyrTrpSerGlnAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu  139
     |||||||||||||||||||||||||||||||||
 401 ATTATTGGAGTCAAAACCTTTTCCAGTGCTTCAATTGCACCCTGTGCCTC  450

 140 AsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCysTh  156
     |||||||||||||||||||||||||||||||
 451 AATGGGACAGTTCACCTCTCTTGTCAGAAAAAACAGAACACAGTGTGCAC  500

 156 rCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerA  173
     |||||||||||||||||||||||||||||||||
 501 CTGCCACGCAGGTTCTTTCTTAGAGAAAACGAGTGTGTCTCGTGTAGTA  550

 173 snCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu  189
     ||||||||||||||||||||||||||||||||||||
 551 ACTGTAAGAAAGCCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG  600

 190 AsnValLysGlyThrGluAspSerGlyThrThr  200
     |||||||||||||||||||||||
 601 AATGTTAAGGGCACTGAGGACTCAGGCACTACA  633
```

seq_name: US-09-525-998A-12.pep proseq.QS:reseqpn/Val1092 nam.AAQ20973

seq_documentation_block:
ID AAQ20973 standard; DNA: 2062 BP.
XX
AC AAQ20973;
XX
DT 11-MAY-1992 (first entry)
XX
DE TNF-alpha binding protein gene.
XX
KW Tumour necrosis factor alpha; autoimmune diseases; cachectin; ss:
KW extracellular domain.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   155..1522
FT   /*tag- a
FT sig_peptide   155..274
FT   /*tag- b
FT mat_peptide   275..1522
FT   /*tag- c
FT misc_feature   473..532
FT   /*tag- d
FT misc_feature   242..751
FT   /note "homologous to probe AAQ20974"
FT   /*tag c
FT   /note "encodes the extracellular domain of human
FT   TNF alpha receptor"
XX
PN GB2246569-A.
XX
PD 05-FEB-1992.
XX
PF 15-JUN-1990;   90GB-0013410.
XX
PR 15-JUN-1990;   90GB-0013410.
XX
PA (CHAR-) CHARING CROSS SUNLE.
XX
PI Feldman M, Gray P, Turner M, Brennan F;
XX
DR WPI; 1992-043613/06.
DR P-PSDB; AAR20787.
XX
PT New tumour necrosis factor alpha binding protein and polypeptide
PT - useful in treating cachexia, sepsis and auto immune diseases
PT e.g. rheumatoid arthritis
XX
PS Disclosure; Fig 1; 25pp; English.
XX
CC The sequence is that of DNA encoding tumour necrosis factor alpha
CC binding protein which was obtd. from a human placental cDNA library
CC in lambda gt11 using a probe (AAQ20974). The DNA also encodes the
CC extracellular domain of human TNF alpha receptor and as such it is
CC useful for treating diseases where TNF alpha is involved as a
CC causative agent, e.g. cachexia, sepsis and autoimmune diseases,
CC specifically rheumatoid arthritis. See also AAQ20974.
XX
SQ Sequence 2062 BP: 429 A, 616 C, 573 G, 444 T, 0 other:

alignment_scores:
Quality: 1117.50   Length: 211
Ratio: 5.588   Gaps: 1
Percent Similarity: 94.787   Percent Identity: 94.787

alignment_block:
US-09-525-998A-12 x AAQ20973

Align seq 1/1 to: AAQ20973 : from: 1 to: 2062

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   1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGl  17
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 155 ATGGGCCTCCACCGTGCCTGGACCTGCTGCTGCCGCTGGTGCTCCTGGA  204

  17 uLeuLeuValGlyIleThrProSerGlyValIleGly............  29
     |||||||||||||||||||||||||
 205 GCTGTTGGTCTGGCAATAACCCCTTCAGGTGTCATTGGTCCCTCACC  254

  30 ............AspSerValCysProGlnGlyLysTyrIle  39
     ||||||||||||||||||||||||||||||
 255 TAGGGGACAGGGAGAAGAGAATAGTCCCAAGGAAAATAATC  304
```

```
seq_documentation_block:
ID   AAQ24440 standard: DNA: 2062 BP.
XX
AC   AAQ24440;
XX
DT   05-NOV-1992 (first entry)
XX
DE   Encodes TNF-alpha 55kD receptor.
XX
KW   tumour necrosis factor alpha; extracellular binding domain;
KW   treatment; pulmonary diseases; septic shock; HIV infection; AIDS;
KW   malaria; viral meningitis; graft versus host disease;
KW   autoimmune disease; rheumatoid arthritis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             156..1517
FT                   /*tag=  a
FT   mat_peptide     1265..1267
FT                   /*tag=  b
FT                   /note= "3"
FT   mat_peptide     1265..1267
FT                   /*tag=  c
FT                   /codon_seq: "TGG", aa:Trp
FT   mat_peptide     1258..1260
FT                   /*tag=  d
FT                   /codon_seq: "AAC", aa:Leu
FT   mat_peptide     1433..1435
FT                   /*tag=  e
FT                   /codon_seq: "AAC", aa:Asn
FT   sig_peptide     156..274
FT                   /*tag=  1
XX
RN   W99207075-A.
XX
PN   30-APR-1992.
XX
PD   18 OCT 1991   91WO-GB01826.
XX
PP   18-OCT-1990   99GB-0922648.
XX
PA   (CRAR-) CHARING CROSS SUNLEY RES CENL.
XX
PI   Brennan FM,  Feldmann M,  Gray PW,  Turner MJC.
XX
DR   AAR24000.
DR   P-PSDB; AAR24000.
XX
PT   New polypeptide capable of binding human TNF alpha - comprises
PT   first three cysteine-rich subdomains of TNF alpha receptor for
PT   treating autoimmune disease, septic shock, HIV etc.
XX
PS   Claim 4; Fig 1; 43pp; English.
XX
CC   This sequence encodes human TNF-alpha 55kD receptor . A placenta cDNA
CC   library in ... was screened with probe AAQ2524. Ten hybridising clones
CC   were plaque purified and cDNA size determined by PAGE against an
CC   Eco RI digested phage DNA. The inserts of the cDNA clones were then
CC   sequenced. The coding region of the majority of the human TNF-alpha
CC   55kD receptor was isolated as an mRNA fragment encoding 374 amino
CC   acids, and cloned into a mammalian cell expression vector, resulting
CC   in TNFR. A derivative of the TNF-alpha receptor was produced by
CC   engineering a termination codon just prior to the transmembrane
CC   domain ... with primers AAQ29297.9 generated a 300bp
CC   restriction fragment which was cloned into pTNFR, giving pTNFRecd.
CC   DNA sequencing confirmed this contained the designed DNA sequence.
CC   The TNF-alpha receptor expression plasmids were then transfected
CC   into monkey COS-7 cells.
CC   See also AAQ24440-51, AAP24000, AAP24089-94, AAP-2985, AAQ2246-8
XX
SQ   Sequence 2062 BP: 429 A; 618 C; 572 G; 443 T; 0 other;
```

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alignment_scores:
        Quality:   2117.50              Length:    211
        Ratio:     5.588                Gaps:      1
Percent Similarity:  91.797    Percent Identity:  94.787

alignment_block:
US-09-525-998A-12 x AAQ24440

Align seq 1/3 to: AAQ24440   from: 1 to: 204
```

```
  1  MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGlu  17
     |||||||||||||||||||||||||||||||||||||||||||||||||||
155  ATGGGCCTCTCAACGGTGCCAGACTTGCTGCTGCCGCTGGTGCTCCTGGA  204

 17  GluLeuValGlyIleTyrProSerGlyValIleGly  29
     ||||||||||||||||||||||||||||||||||||
205  GCTGTTGGGCATATACCCGAGCGGGGTCATCGGCGAG  254

 30  .................AspSerValLysProGlnGlyLysTyrIle  38
                     |||||||||||||||||||||||
255  TAGCGGCATAGGGAGAAGACAAGAATGAGGTCGTGCCCAAGAAAATAATT  304

 40  HisProGlnAsnAsnSerIleCysCysThrLysCysHisLysGlyThr  56
     |||||||||||||||||||||||||||||||||||||||||||||||||
305  CACCCTCAAAATAATTCAATTTGTTGTACTAAATGCCATAAAGGAACTA  354

 56  IleLeuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArgGluC  73
     ||||||||||||||||||||||||||||||||||||||||||||||||||||
355  ...
```

```
CC   The sequence encodes the entire 30 kD TNF inhibitor. The clone from
CC   which the sequence was obtd. was isolated from a cDNA library
CC   prepd from RNA from m937 cells treated with PMA/PHA.   The whole
CC   gene can be inserted into expression vectors for prepn. of TNF
CC   inhibitor for use in the treatment of inflammatory and degenerative
CC   diseases.
CC   See also AAQ10878, AAQ10884 and AAQ10907.
XX
SQ   Sequence 2088 BP; 439 A, 626 C, 578 G, 445 T, 0 other;
```

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alignment_scores:
                Quality:  1117.50           Length:       211
                Ratio:       5.588          Gaps:           1
Percent Similarity:  94.787     Percent Identity:  94.787
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alignment_block:
US-09-525-998A-12 x AAQ10883

Align seg 1/1  to: AAQ10883    ...    from:  1  to: 2088

  1 MetGlyLeuSerThrValProAspLeuLeuValLeuLeuGl  17
    |||||||||||||||||||||||||||||||||||||||||
169 ATGGGCCTCTCCACCGTGCCCGACCTGCTGGTGCTCCTGGA  218

 17 uLeuLeuValGlyIleTyrProSerGlyValIleGly..........  29
    ||||||||||||||||||||||||||||||||
219 GCTGTTGGTGGGAATATCCCCTCAGGGGTTATTGGA  268

 30              AspSerValCysProGlnGlyLysTyrIle  39
                ||||||||||||||||||||||||||
269 TAGGGACAGAGAAAGAGATAGTGTGTCCCCAGGAAAATAATC  318

 40 HisProGlnAsnAsnSerIleCysCysThrLysCysHisLysGlyThrTy  56
    |||||||||||||||||||||||||||||||||||||||||
319 CACCCTCAAAATAATTCGATTTGCTGCACAAAGTGCCACAAAGGAACCTA  368

 56 rLeuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArgGluC  73
    |||||||||||||||||||||||||||||||||||||||||
369 CTTGTACAATGACTGCCCAGGCCCAGGTCAGGATACTGACTGCAGGGAGT  418

 73 ysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu  89
    |||||||||||||||||||||||||||||||||||||||||
419 GTGAGAGCGGGTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC  468

 90 SerTyrSerLysLysArgLysGlnMetGlyCysGlyCysSerArgLysSerCy  106
    |||||||||||||||||||||||||||||||||||||||||
469 AGCTACTCTAAAAGGAAGAGAAAGCAGATGTGCGGCTGCTCTCGG  518

106 sThrValAspArgAspThrValCysGlyCysSerArgLysSerGlnTyrArgH  123
    |||||||||||||||||||||||||||||||||||||||
519

123 isThrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu  139
    |||||||||||||||||||||||||||||||||||||||||
569 ATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGTCTGTGCCTC  618

140 AsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCysTh  156
    |||||||||||||||||||||||||||||||||||||||||
619 AATGGGACCGTGCACTCTCTGCCAGGAAAAGCAGAACACCGTGCAC  668

156 rCysHisAlaGlyPheGluArgGluAsnGluCysValSerCysSerA  173
    |||||||||||||||||||||||||||||||||||||||||
669 CTGTCATGCAGGTTTCTTCTAAGAGAAAACGAGTGTCCTCCTGTAGTA  718

173 snCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu  189
    |||||||||||||||||||||||||||||||||||||||||
719 ACTGTAAGAAAAGCCTCGAGTGCACGAAGTTCCTGCCCCAGATTGAG  768

189 AsnValLysGlyThrGluAspSerGlyThrTh  200
    ||||||||||||||||||||||
769 AATGTTAAGGGCACTGAGGACTCAGGGACCACA  801
```

```
355 CTTGTACAATGACTGCCCAGGCCCAGGTCAGGATACTGACTGCAGGGAGT  404
 74 ysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu  89
    |||||||||||||||||||||||||||||||||||||||||
405 GTGAGAGCGGGTCTTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC  454

 90 SerTyrSerLysLysArgLysGlnMetGlyCysGlyCysSerArgLysSerCy  106
    |||||||||||||||||||||||||||||||||||||||||
455 AGCTACTCTAAAAGGAAGAGAAAGCAGATGTGCGGCTGCTCTCGG  504

106 sThrValAspArgAspThrValCysGlyCysSerArgLysSerGlnTyrArgH  123
    |||||||||||||||||||||||||||||||||||||||
505 CACAGTGGACACCCGGACACCGTGTGCGGCTGCTCCAGGAAAAGCCAGTACCGGC  554

123 isThrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu  139
    |||||||||||||||||||||||||||||||||||||||||
555 ATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGTCTGTGCCTC  604

140 AsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCysTh  156
    |||||||||||||||||||||||||||||||||||||||||
605 AATGGGACCGTGCACTCTCTGCCAGGAAAAGCAGAACACCGTGCAC  654

156 rCysHisAlaGlyPheGluArgGluAsnGluCysValSerCysSerA  173
    |||||||||||||||||||||||||||||||||||||||||
655 CTGTCATGCAGGTTTCTTCTAAGAGAAAACGAGTGTCTCCTGTAGTA  704

173 snCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu  189
    |||||||||||||||||||||||||||||||||||||||||
705 ACTGTAAGAAAAGCCTCGAGTGCACGAAGTTCCTGCCCCAGATTGAG  754

189 AsnValLysGlyThrGluAspSerGlyThrTh  200
    ||||||||||||||||||||||
755 AATGTTAAGGGCACTGAGGACTCAGGGACCACA  787
```

```
seq_name. ...
seq_documentation_block:
ID   AAC83946 standard: DNA: 2088 BP.
XX
AC   AAC83946;
XX
DT   02-MAR-2001 (first entry)
XX
DE   Human 30 kDa TNF inhibitor precursor coding sequence.
XX
KW   TNF inhibitor, antiinflammatory, Tumour Necrosis Factor; interleukin;
KW   IL-1; inflammatory disease; degenerative disease; human; ss.
OS   Homo sapiens.
XX
PN   US6143866-A.
XX
PD   07-NOV-2000.
XX
PF   19-JAN-1995;    95US-0375242.
XX
PR   19-JUL-1990;    90US-0555274.
PR   09-JUL-1993;    93US-0090466.
PR   18-JUL-1989;    89US-0381080.
PR   11-DEC-1989;    89US-0450329.
PR   07-FEB-1990;    90US-0479661.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Squires C, King MW, Hale KK, Brewer MT, Thompson RC;
PI   Vanderslice RW, Vannice J, Kohno T;
XX
DR   WPI, 2001-06444/61.
DR   P-PSDB: AAB37677.
XX
PT   Novel 30 kDa tumor necrosis factor inhibitor analog comprising a
PT   non-native cysteine residue cross linked with polyethylene glycol,
PT   useful for treating inflammatory and degenerative diseases mediated by
PT   TNF -
XX
PS   Example 6; Fig 21; 82pp; English.
XX
CC   The present invention relates to Tumour Necrosis Factor (TNF) inhibitors
CC   (see AAB37676 and AAB37685), which have TNF inhibitory activity. The
CC   novel TNF inhibitors of the present invention are useful as therapeutic
CC   agents for inhibiting the activity of TNF and interleukin (IL-1), and
CC   for treating inflammatory and degenerative diseases mediated by TNF. The
CC   present sequence is the coding sequence for the precursor of 30 kDa TNF
CC   inhibitor. The 30 kDa TNF inhibitor can inhibit TNF alpha.
XX
SQ   Sequence 2088 BP; 439 A; 626 C; 578 G; 445 T; 0 other;
```

```
alignment_scores:
       Quality: 1117.50        Length:       211
         Ratio: 5.588            Gaps:         1
Percent Similarity: 94.787    Percent Identity: 94.787
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alignment_block:
US-09-525-998A-12 x AAC83946
Align seq 1/1 to: AAC83946 1/528; 1 to: 2088
```

```
    1 MetGlyLeuSerThrValProAspLeuLeuProLeuValLeuLeuGl 17
      |||||||||||||||||||||||||||||||||||||||||||||||
  169 ATGGGGCTCTCCACCGTCCCAGACCTGCTGCCCCTGGTGCTCCTGGA 218

   17 uLeuLeuValGlyIleTyrProSerGlyValIleGly...          29
      |||||||||||||||||||||||||||||||||||||
  219 GTTGTTGGTGGAAATAACCCAGAGCGGAATAGGAATAGGAATCTAACG...  268

   30 ...............AspSerValCysProCysGlyCysTyrIle 39
```

```
269 TAGGGGCACAGGAGAACGACATAGTGTGTCCCTGCAAGAAAATATAG    318
    |||||||||||||||||||||||||||||||||||||||||||||||
 40 HisProGlnAsnAsnSerIleCysCysThrLysCysHisLysGlyThr    56
    |||||||||||||||||||||||||||||||||||||||||||||||
319 CACCCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGCAACCCA  368

 56 ThrLysAspAspTyrProGlyProGlnAspAsnAspAspCysArgGl    74
    |||||||||||||||||||||||||||||||||||||||||||||||
369 CTTGTACAATGA TGTGAGGGACAGGACAGTAGACATGGACGGGAGT  418

 74 TyrGlnSerGlySerPheThrAlaSerGlnAspAsnHisSerArgHisCys    89
    |||||||||||||||||||||||||||||||||||||||||||||||||||
419 GTGCAGAGCGGCTCCTTCACCGCTTCAGAAGACAACCACAGACAGCACTGC   468

 90 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCys    106
    |||||||||||||||||||||||||||||||||||||||||||||||||||
469 AGCTGCTCCAAAGTGCCAAAGGAAATGGGCAAGTGGAGATCAGCTCCTGC   518

106 SerThrValAspArgAspThrValCysGlyCysArgGlyAsnIleTyrArg    123
    |||||||||||||||||||||||||||||||||||||||||||||||||||
519 CACAGTGGACGGGAATATAACGTCTGTGGTGCAGGAGGAACGGGC  568

123 IleTyrTrpSerGlnAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu    139
    |||||||||||||||||||||||||||||||||||||||||||||||||||
569 ATTATTGGTCAGAACCTTCCAGTGCTTCAATGTTCACTGTGTCAGCTGC  618

140 AsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCysTh    156
    ||||||||||||||||||||||||||||||||||||||||||||||||||
619 AATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAACAACGTGTGTGCAC   668

156 ThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerAsn    173
    |||||||||||||||||||||||||||||||||||||||||||||||||||
669 ACTTGTCATGCAGGGTTCTTTCTCAGAGAAAATGAGTGTGTGAGTGGTAGTA   718

173 SerCysLysSerGlyCysThrTyrSerCysLeuProGlnIleGlnIleGln    189
    |||||||||||||||||||||||||||||||||||||||||||||||||||
719 AGTGTAAGAGTGGGTGCACGTACAGTTGCCTACCGCAGATTCAG   768

190 AsnValGlyThrGluAspSerGlyThrThr    200
    ||||||||||||||||||||||||||||||
769 AATGTTAAGGCACTGAGGACTGAGGACCCATA   801
```

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seq_name. ...
seq_documentation_block:
ID   AAQ10955 standard: cDNA: 2111 BP.
XX
AC   AAQ10955;
XX
DT   24-MAY-1991 (first entry)
XX
DE   Encodes human 55kD TNF-binding protein.
XX
KW   Tumour Necrosis Factor, binding protein; septic shock;
KW   autoimmune glomerulonephritis; lymphokine; cytokine.
XX
FH   Key              Location/Qualifiers
FT   sig_peptide      187..273
FT                    /tag= a
FT   mat_peptide      274..1551
FT                    /tag= b
XX
PN   EP417563-A.
XX
PD   20-MAR-1991.
XX
PF   31-AUG-1990.    90EP-0116787.
XX
PR   20-APR-1990;    90CH-0001347.
PR   12-SEP-1989;    89CH-0003419.
PR   08-MAR-1990;    90CH-0000746.
```

XX
PA   (HOFF) HOFFMANN-LA ROCHE AG.
XX
PI   Brockhaus M., Dembic Z., Gentz R., Lesslauer W., Lotscher H;
PI   Schlaeger EJ;
XX
DR   WPI; 1991-081851/12.
DR   P-PSDB; AAR11082.
XX
PT   Insoluble tumour necrosis factor binding proteins - and DNA
PT   encoding them, useful in pharmaceutical prods. and for antibody
PT   prodn.
XX
PS   Claim 4; Fig 1; 26pp; German.
XX
CC   Partial amino acid sequences were determined for the 55 and 75kD
CC   TNF-BPs (see AAP11072-P11081) and oligonucleotide primers were
CC   synthesised based on these partial sequences. The primers were used
CC   to produce a cDNA fragment for use as a probe to screen a human
CC   placental cDNA bank constructed in lambda gt11. Positive clones were
CC   identified and sequenced. DNA constructs comprising the TNF-BP coding
CC   sequence may also contain a fragment encoding a human Ig domain
CC   Recombinant constructs are used to transform cells to confer
CC   improved TNF-binding properties.
CC   See also AAQ10956.
XX
SQ   Sequence 2111 BP; 445 A; 628 C; 588 G; 450 T; 0 other;

alignment_scores:
          Quality: 1117.50   Length: 211
          Ratio: 5.588   Gaps: 1
     Percent Similarity: 94.787   Percent Identity: 94.787

alignment_block:
US-09-525-998A-12 x AAQ10955

Align seq 1/1   to: AAQ10955   from: 1 to: 2111

  1 MetGlyLeuSerThrValProAspLeuLeuLeuProLeuValLeuLeuGl 17
    |||||||||||||||||||||||||||||||||||||||||||||||||||
187 ATGGGCCTCTCAACGGTGCCGGACCTGCTGCTGCCGCTGGTGCTCCTGGCA 236

 17 uLeuLeuValGlyIleTyrProSerGlyValIleGly.............. 29
    |||||||||||||||||||||||||||||
237 GTGTTGGTAGGAATAIATCCTTCAGGAGTIATIGGAIGGTGGTCATCAAT 285

 30 ....AspSerValCysProGlnCysTyrTyrIle 39
              ||||||||||||||||||||||||||||
287 TAGGGACACGGGAGAGAGATATGTCGTGCCCCCAAGGAAAATATATC 336

 40 HisProGlnAsnAsnSerIleCysCysThrLysCysHisLysGlyThrTy 56
    |||||||||||||||||||||||||||||||||||||||||||||||||
337 CACCCTCAAAAIAAIICGAIIIGCIGIACCAAGIGCCACAAAGGAACCTA 386

 56 rLeuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArgGluC 73
    ||||||||||||||||||||||||||||||||||||||||||||||||||
387 CTTGTACAATGACTGTCCAGGCCCGGGTCAGGATACGGACTGTAGGAGT 436

 73 ysGluSerGlySerThrAlaSerGluAsnHisLeuArgHisCysLeu 89
    |||||||||||||||||||||||||||||||||||||||||||||||
437 GTGAGAGCGGGTCCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 486

 90 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCy 106
    ||||||||||||||||||||||||||||||||||||||||||||||||||
487 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTTG 536

106 sThrValAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgH 123
    |||||||||||||||||||||||||||||||||||||||||||||||||
537 CACAGTGGATCGAGACACTGTATGTGGCTGTCGAAAGAACCAGTACCGGC 585

123 isTyrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu 139
    |||||||||||||||||||||||||||||||||||||||||||||||||

```
CC    glomerulonephritis, cerebral malaria, immune responses and inflammation),
CC    (ii) to purify TNF, (iii) to identify TNF (antagonists and (iv) for
CC    diagnostic determination of TNF in body fluids. Antibodies raised against
CC    (I) are used for affinity purification of (I). This sequence encodes
CC    a tumour necrosis factor binding protein described in the method of
CC    the invention.
XX
SQ    Sequence 2111 BP; 445 A; 629 C; 587 G; 450 T; 0 other;

alignment_scores:
          Quality:   1117.50          Length:     211
          Ratio:     5.588            Gaps:         1
Percent Similarity:  94.787   Percent Identity:  94.787

alignment_block:
US-09-525-998A-12 x AAZ09170

Align seq 1/1  to: AAZ09170  from: 1  to: 2111

  1 MetGlyLeuSerThrValProAspLeuLeuProLeuValLeuLeuGl 17
    ||||||||||||||||||||||||||||||||||||||||||||||||
187 ATGGGCCTCTCCACGGTGCCTGACCTGCTGCCGCTGGTGCTACTGGA 236

 17 uLeuLeuValGlyIleTyrProSerGlyValIleGly............... 29
    ||||||||||||||||||||||||||||||
237 GCTGTTGGTGGGAATATACCCTCAGGGTATTGGACTGTGCCTCACC 286

 30 ..................AspSerValCysProGlnGlyLysTyrIle 39
                      ||||||||||||||||||||||||||||||
287 TAGGGGACAGGGAGAAGAGACATACGTGTCCCCAAGGGAAATATATC 336

 40 HisProGlnAsnAsnSerIleCysCysThrLysCysHisLysGlyThr 55
    ||||||||||||||||||||||||||||||||||||||||||||||||
337 CACCCTCAAAATAATTCGATTTGTTGTACAAAGTGTCATAAAGGAACTA 485

 56 TyrTyrAsnAspThrTyrCysThrAspGlyAspThrAspCysArgGluC 73
    ||||||||||||||||||||||||||||||||||||||||||||||||
387 CTTGTATAATGATACGTACTGCACGGATGGAGATACAGACTGCAGGGAGT 436

 73 ysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 89
    ||||||||||||||||||||||||||||||||||||||||||||||||
437 GTGAGAGCGGGTCCTTCACCGCTTCAGGAAAACCACCTCAGACACACCCTC 486

 90 SerCysSerLysCysArgLysGluMetGlyGlnValGlnIleSerSerCy 106
    ||||||||||||||||||||||||||||||||||||||||||||||||
487 AGTTGTTCTAAATGCCGAAAAGAAATGGGTCAGGTACAAATTTCTTCTTG 536

106 sThrValAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgH 123
    ||||||||||||||||||||||||||||||||||||||||||||||||
537 CACAGTGGATCGAGACACCGTGTGTGGCTGTAGGAAAAACCAGTACCGGC 585

123 isTyrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu 139
    ||||||||||||||||||||||||||||||||||||||||||||||||
587 ATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTC 636

140 AsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCysTh 156
    ||||||||||||||||||||||||||||||||||||||||||||||||
637 AATGGGACCGTCCACCTGAGCTGCCAGGAAAAACAGAACACGGTGTGCAC 686

156 rCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerA 173
    ||||||||||||||||||||||||||||||||||||||||||||||||
687 CTGCCATGCAGGGTTTTTCCTAAGAGAAAATGAGTGTGTCTCCTGTAGTA 736

173 snCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 189
    ||||||||||||||||||||||||||||||||||||||||||||||||
737 ACTGTAAGAAAAGCCTGGAGTGCACAAAGTTGTGCCTACCCCAGATTGAG 786

190 AsnValProGlyThrGluAspSerGluThrThr 200
    |||||||||||||||||||||||||||||||||
787 AATGTTAAGGGCACTGAGGACTCAGGCCACCACA 819

seq_name: ... NA ... AAZ48475
```

```
seq_documentation_block:
ID    AAZ48475; standard; RNA; 2161 BP.
XX
AC    AAZ48475;
XX
DT    31-MAR-2000  (first entry)
XX
DE    Human tumour necrosis factor receptor (TNFR1) nucleotide sequence.
XX
KW    Tumour necrosis factor receptor type 1, TNFR1, antisense, infection;
KW    inflammation, tumour formation; TNFR1 antagonist; ds.
XX
OS    Homo sapiens.
XX
PN    US6007995-A.
XX
PD    28-DEC-1999.
XX
PF    26-JUN-1998;  98US 0106038.
XX
PR    26-JUN-1998;  98US-0106038.
XX
PA    (ISIS-) ISIS PHARM INC.
XX
PI    Baker BF, Cowsert LM;
XX
DR    WPI: 2000-185443/09.
XX
PT    Antisense inhibition of tumor necrosis factor type 1 expression for
PT    diagnosis, treatment and prevention of disease, particularly tumors -
XX
CC    Example 10, Columns 33-35; 34pp; English.
XX
CC    The invention provides antisense compounds targeted to human tumour
CC    necrosis factor receptor type 1 (TNFR1) RNA, these antisense compounds
CC    can be used in a method of inhibiting the expression of TNFR1 human cells
CC    or tissues. The antisense compounds specifically hybridize with one or
CC    more nucleic acids encoding TNFR1 modulating the function of nucleic
CC    acid molecules encoding TNFR1, ultimately modulating the amount of TNFR1
CC    produced. The antisense compounds and method are useful as research
CC    reagents and diagnostics, and in the treatment and prophylaxis of
CC    infection, inflammation, or tumour formation. The present sequence
CC    represents the nucleotide sequence of human TNFR1 (GenBank Accn No:
CC    X55313).
XX
SQ    Sequence 2161 BP; 459 A; 642 C; 604 G; 456 T; 0 other;
```

```
alignment_scores:
          Quality:   1117.50          Length:     211
          Ratio:     5.588            Gaps:         1
Percent Similarity:  94.787   Percent Identity:  94.787

alignment_block:
US-09-525-998A-12 x AAZ48475

Align seq 1/1  to: AAZ48475  from: 1  to: 2161

  1 MetGlyLeuSerThrValProAspLeuLeuProLeuValLeuLeuGly 17
    ||||||||||||||||||||||||||||||||||||||||||||||
256 ATGGGCCTCTCCACGGTGCCTGACCTGCTGCCGCTGGTGCTGCTGGGA 405

 17 uLeuLeuValGlyIleTyrProSerGlyValIleGly............... 29
    ||||||||||||||||||||||||||||||
306 GCTGTTGGTGGGAATATACCCTCAGGGTATTGGACTGTGCCTCACC 455

 30 ..................AspSerValCysProGlnGlyLysTyrIle 39
                      ||||||||||||||||||||||||||||
356 TAGGGGACAGGGAGAAGAGACATACGTGTCCCCAAGGGAAATATATC 405

 40 HisProGlnAsnAsnSerIleCysCysThrLysCysHisLysGlyThr 54
    ||||||||||||||||||||||||||||||||||||||||||||||
```

PI   Batkin M, Brakebusch C, Varlolomeev E, Wallach D;
XX
DR   WPI; 1995-194342/26.
DR   P-PSDB; AAR75084.
XX
PT   New protease capable of cleaving soluble tumour necrosis factor
PT   (TNF) receptor - from cell-bound TNF- receptor, useful for
PT   antagonising deleterious effects of TNF.
XX
PS   Disclosure; Fig 1; 40pp; English.
XX
CC   This sequence represents human p55 tumour necrosis factor (TNF-R) DNA.
CC   Expression of this receptor is regulated by shedding of the
CC   extracellular receptor fragment. The p55 TNF-R can be shed in response
CC   to different inducing agents, e.g. phorbol myristate acetate (PMA),
CC   depending on cell type. The only region of the receptor whose structure
CC   affects the shedding response is the spacer region (see AAR75012) in the
CC   extracellular domain. This region is located close to a site of cleavage
CC   of the molecule, and links the Cys rich module to the transmembrane
CC   domain. The spacer region of the encoded protein was used to create the
CC   chimeras between human p55 TNF-R and murine epidermal growth factor
CC   receptor (EGF R) that are represented by AAR75007-11. This spacer region
CC   was subjected to deletion mutations (AAR75013-25) and substitutions
CC   (AAR75026-47), of the spacer region, the most important residues are
CC   Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
CC   important of these. The shedding of the receptor is independent of the
CC   side chain identity of these residues, with the exception of a limited
CC   dependence on the identity of Val 173. Mutations which alter the
CC   conformation of the protein adversely effect the shedding process. The
CC   mutations shown in AAR75013-47 were introduced in order to create an
CC   inhibitor of a protease that is capable of cleaving the soluble TNF-R
CC   from the cell bound TNF-R. Fragments of these inhibitors can be seen in
CC   AAR75017-9, AAR75025, AAR75033-5 and AAR75042-3. These protease
CC   inhibitors can be used for enhancing TNF function.
XX
SQ   Sequence 2175 BP; 474 A; 642 C; 603 G, 456 T; 0 other;

alignment_scores:
         Quality: 1117.50   Length: 211
         Ratio: 5.588   Gaps: 1
Percent Similarity: 94.787   Percent Identity: 94.787

alignment_block:
US-09-525-998A-12 x AAQ90513

Align seq 1/1   to: AAQ90513   from: 1 to: 2175

   1 MetGlyLeuSerThrValProAspLeuLeuProLeuValLeuLeuGl 17
     |||||||||||||||||||||||||||||||||||||||||||||||
 256 ATGGGACTCTCAACGGCACTGACCTGGAGCTGCTGCCTCTGGTGCTCCTGGA 305

  17 uLeuLeuValGlyIleTyrProSerGlyValIleGly............... 29
     ||||||||||||||||||||||||||||||
 306 GCTGTTGGTGGGAATATACCCTAGTGGTTATTGGAGTGGTCCCTACC 355

  29 ....AspSerValCysProGlnGlyLysTyrIle 39
                             ||||||||||||||||||||||||
 356 TAGGGCACAGCGAACAAGAGATACTGTGTCCCCAAGGAAAATATATC 405

  40 HisProGlnAsnAsnSerIleCysCysThrLysCysHisLysGlyThrT 56
     |||||||||||||||||||||||||||||||||||||||||||||||
 406 CACCCTCAAAATAATTCGATTTGCTGCACAAGTGCCACAAGGAACCTA 455

  56 rLeuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArgGluC 73
     |||||||||||||||||||||||||||||||||||||||||||||||
 456 CTTGTACAACGACTGCCCAGGGCCAGGACAGGATACTGACTGCAGGGAGT 505

  73 ysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 89
     |||||||||||||||||||||||||||||||||||||||||||||||
 506 GTGAGAGCGGCTCCTTCACCGCTAGCGAAAACCACCTCAGACACTGCCTC 555

  90 SerCysSerLysCysArgLysGluMetGlyGlnValGlnIleSerSerCy 106
     |||||||||||||||||||||||||||||||||||||||||||||||
 556 AGCTGCTCCAAATGCCGAAAGGAAATGGGTCAGGTGCAGATCTCTTCTTG 605

 106 sThrValAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgH 123
     |||||||||||||||||||||||||||||||||||||||||||||||
 606 CACAGTGGACCGGGACACGGTCTGCGGCTGCCGCAAGAACCAGTACCGCC 655

 123 isTyrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu 139
     |||||||||||||||||||||||||||||||||||||||||||||||
 656 ATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTC 705

 140 AsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCysTh 156
     |||||||||||||||||||||||||||||||||||||||||||||||
 706 AATGGGACGGTACATCTGTCATCACAGGAAAAGCAAAATACGGTGTGAC 755

 156 rCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerA 173
     |||||||||||||||||||||||||||||||||||||||||||||||
 756 CTGCCATGCAGGTTTCTTCCTAAGAGAAAACGAGTGTGTCTCCTGTAGTA 805

 173 snCysLysLysSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 189
     |||||||||||||||||||||||||||||||||||||||||||||||
 806 ACTGCAAGAAAAGCCTGGAGTGCACGAAGTTGTGCCTACCCCAGATTGAG 855

 190 AsnValLysGlyThrGluAspSerGlyThrThr 200
     |||||||||||||||||||||||||||||||||
 856 AATGTTAAGGGCACTGAGGACTCAGGACCACCA 888

seq_name: US-09-525-998a-12 ... Standard; DNA ... SA: AAQ90513

seq_documentation_block:
ID   AAQ90513 standard; DNA; 2175 BP.
XX
AC   AAQ90513;
XX
DT   19-JAN-1996 (first entry)
XX
DE   p55 TNF-R gene.
XX
KW   p55, tumour necrosis factor receptor; TNF-R; human; murine; chimera;
KW   epidermal growth factor receptor; EGF-R, protease; inhibitor;
KW   phorbol myristate acetate; PMA; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   256..1623
FT   /*tag-   a
FT   /product- p55 TNF-R
FT   misc_signal   2143..2149
FT   /*tag-   b
FT   /note- "possible poly-A signal"
XX
PN   AU9175742-A.
XX
PD   04-MAY-1995.
XX
PF   11 OCT-1994; 94AU-0075742.
XX
PR   12-OCT-1993; 94IL-0107268.
XX
PA   (YEDA) YEDA RES & DEV CO LTD.
XX

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CC    pools).
SO    Sequence 6889 BP; 1729 A; 1826 C; Bgl G; 1614 T; 0 other;

alignment_scores:
          Quality:  1117.50        Length:     211
          Ratio:    5.588          Gaps:
      Percent Similarity:  91.787   Percent Identity:  91.787

alignment_block:
  US-09-525-998A-12 x AAI15931

Align seg 1/1   to: AAI15931    from:  1   to: 6889

   1 MetGlyLeuSerThrValProAspLeuLeuProLeuValLeuLeuG; 17
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1605 ATGGGCCTCTCCACCGTGCCTGACCTGCTGCCGCTGGTGCTCCTGGA 1654

  17 uLeuLeuValGlyLleTyrProSerGlyValGly.............. 29
     |||||||||||||||||||||||||||||||||
1655 GCTGTTGGTGGGAATATACCCCAGGGGATTGGA TGGTCCTCACG 1704

  30 .....................AspSerValCysProGlnGlyLysTyrIle 39
                         |||||||||||||||||||||||
1705 TAGGGCAGGTGAGAAGAGAGATAGTGTGTCCCCAAGGAAAA AATAAT 1754

  40 HisProGlnAsnAsnSerIleCysCysThrLysCysHisLysGlyThrTy 56
     ||||||||||||||||||||||||||||||||||||||||||||||
1755 CACCCTCAAAATAATTGATTTGCTGTACCAAGTGCCACAAGGAAGGAACCTA 1804

  56 rLeuTyrAsnAspTyrSerGlyPheGlyThrMetAspThrAspTyrSerGly 73
     |||||||||||||||||||||||||||||||||||||||||||||||
1805 CTTGTACAATGACTGTCCAGGAGGGGGAACAATGGACACAGATTAC AGT 1854

  73 ysGluSerGlySerPheThrAlaSerGlnAsnHisLeuArgHisLysSer 89
     |||||||||||||||||||||||||||||||||||||||||||||||
1855 GTGAGAGCGGGTCCTTCACCGTGCTCAGCAAAACCACCTCAGACACTGCCTC 1904

  90 SerCysSerLysSerValArgLysGluMetGlyGlnValGlnIleSerSerGly 106
     |||||||||||||||||||||||||||||||||||||||||||||||
1905 AGCTGCTCAAAGTCCGAAAGGAAATGGGTCAGGTGCAGAT TCTTCTTG 1954

 106 sThrValAspProAspThrValCysGlyCysArgLysAsnGlnTyrArgH 123
     |||||||||||||||||||||||||||||||||||||||||||||||
1955 CAACTGGA GAAAACCGTGTGGGGTGCAGAAA AATC AGTACCGA 2004

 123 isTyrTrpSerGluAsnLeuPheGlnCysProSerLeuCysLeu 139
     |||||||||||||||||||||||||||||||||||||||
2005 ATTATTGGAGTGAAAACCTTTCCAGTGCCCTCAATTGCAGTCTGCCTC 2054

 140 AsnGlyThrValHisLeuSerCysGlnLeuAsnThrValCysTh 156
     |||||||||||||||||||||||||||||||||||||||||
2055 AATGGGACCGTGCACCTGTCCTGCCAGGAAACAGAACCGTGTGCAC 2104

 156 rCysHisAspGlyPheLeuAsnGlyAlaGluAsnAspTyrValThrThr 174
     ||||||||||||||||||||||||||||||||||||||||||||
2105 CTGCCATGACGGCTTTCTAAACGGGGCAGAAAACGACTATGTGACAACA 2154

 174 sCysGlyLysLysThrAlaLeuTyrArgGlyGluTyrIleLeu 189
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2155 AGCTGCGGGAAAAAGACGGCACTCTACAGGGGAGAGTACATCCTG 2204

 190 AsnValGlyLysThrArgAspSerGlyThrThr 200
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2205 AATGTTGGGAAGACAAGAGATAGTGGAACAACA 2237

seq_documentation_block:
  ID   AAV04411 standard; DNA; 6926 BP.
  XX
  AC   AAV04411;
  XX
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DT   27-APR-1998 (first entry)
XX
DE   Vector pcDNA3-IgG1-TNF-R.
XX
KW   murine; mouse; immunoglobulin G1; heavy chain; human; chimeric;
KW   vector pcDNA3; IgG1 TNF-R; tumour necrosis factor receptor,
KW   screening; combinatorial library; CH2; CH3; hinge region; ss.
XX
OS   Chimeric - Mus sp.
OS   Chimeric - Homo sapiens
OS   Synthetic.
XX
PN   WO9737220-A1.
XX
PD   09-OCT-1997.
XX
PF   02-APR-1997; 97WO-US05821.
XX
PR   03-APR-1996; 96US-0627151.
XX
PA   (CHUG-) CHUGAI BIOPHARMACEUTICALS INC.
XX
PI   Recherer KA, Brown SJ, Spinella DG;
XX
DR   WPI; 1997-503233/46.
XX
PT   Screening of compounds for ability to bind specific molecules -
PT   using a chimeric protein in which the specific molecule is fused to
PT   an immunoglobulin chain
XX
PS   Example 1; Pages 49-54; 80pp; English.
XX
CC   The present vector, which is designated pcDNA3-IgG1-TNF-R and
CC   contains nucleic acid sequences encoding mouse immunoglobulin G1
CC   (IgG1) CH2, CH3 and hinge regions and the human tumour necrosis
CC   factor receptor, was used in the development of a novel
CC   method of screening compounds for ability to bind a specific
CC   molecule. The method comprises contacting one or more compounds
CC   with a chimeric protein containing at least two domains, the 1st
CC   comprising a portion of the specific molecule, and the 2nd an
CC   immunoglobulin chain portion having one or more epitopes and/or
CC   immunoglobulin regions recognising an epitope. A binding partner
CC   complex between the chimeric protein and compound(s) is formed,
CC   separated out and contacted with a (indirectly labelled secondary
CC   molecule which binds the 2nd domain, and the label detected. Using
CC   the chimeric proteins, compounds can be rapidly screened for
CC   binding to an antigen, antibody, enzyme, enzyme substrate, receptor
CC   or ligand, e.g. in biomedical research and drug development. The
CC   method is especially intended for screening combinatorial
CC   libraries, but is also useful in screening bacterial/phage lysates,
CC   assays requiring specific binding partner interaction and obtaining
CC   binding analogues of a compound.
XX
SQ   Sequence 6926 BP; 1638 A; 1816 C; 1765 G; 1707 T; 0 other;

alignment_scores:
     Quality: 1117.50   Length: 211
     Ratio: 5.588   Gaps: 1
Percent Similarity: 94.787   Percent Identity: 94.787

alignment_block:
US-09-525-998A-12 x AAV04431
Align seq 1/1 to: AAV04431   from: 1 to: 6926

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935 ATGGGCTCTCTACCGTGGGCTCCTCTCGTGTGTGTGTGTGTGTCTGGA 984

 17 gLeuLeuValGlyIleTyrProSerGlyValIleGly............ 29
    ||||||||||||||||||||||||||||||||
985 GCTGTTGGTGGGGAATATACCCCTCAGGGCGGTTATTGGACTGGTCCCTCACC 1034

                         ....AspSerValCysProGlnGlyLysTyrIle 39
                                    |||||||||||||||||||||||||||
  1035 TAGGGCAGGGCAAGGAGTAGTGTGTGGGCCCAAGGAAATATATC 1084

 40 HisProGluAsnAsnSerIleCysCysThrLysCysHisLysGlyThr 56
    |||||||||||||||||||||||||||||||||||||||||||||
1085 CACCCTCAAATAATTCATTTGCTGTACCCAACTGCCACAAGGAACCTA 1134

 56 rLeuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArgGluC 73
    ||||||||||||||||||||||||||||||||||||||||||||||||
1135 CTTGTACAATGACTGTCCAGGCCCGGGCAGGATACGGACTGCAGGGAGT 1184

 73 ysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 89
    |||||||||||||||||||||||||||||||||||||||||||||||
1185 GTGAGAGCGGTTCACTTTCAGAAAACAATCTACATACTGCGTC 1234

 90 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCy 106
    |||||||||||||||||||||||||||||||||||||||||||||||||
1235 AGTTCGTCCAAATGCCGAAAGGAAATGGGTCAGGTGGAGATCTCTTCTG 1284

106 sThrValAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgH 123
    ||||||||||||||||||||||||||||||||||||||||||||||||
1285 CACAGTGGACCGGGACACCGTGTGTGGGTGTCGGCAAGAACCAGTACCGGC 1334

123 isThrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu 139
    |||||||||||||||||||||||||||||||||||||||||||||||||
1335 ATTATTGGAGTGAAAACTTTTCCAGTGTTTCAATTGCAGCCTCTGGCTC 1384

140 AsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCysTh 156
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1385 AAtGGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCAC 1434

156 rCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerA 173
    ||||||||||||||||||||||||||||||||||||||||||||||||
1435 CTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCCTGTAGTA 1484

173 snCysSerSerLeuGluCysThrLysLeuCysLeuProGlnIleGlu 189
    ||||||||||||||||||||||||||||||||||||||||||||
1485 ACTTCTAAGAAAGACCTGAATGTACGAATTGTGTCTACCCAGAATTGAG 1534

190 AsnValLysGlyThrGluAspSerGlyThrThr 200
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1535 AAtGTTAAGGGCACTGAGGACTCAGGCACCACA 1567

seq_name: /SEQDAT/gcqdata/geneseq/geneseqp/NA1993.DAT:AAQ50870

seq_documentation_block:
ID   AAQ50870 standard; DNA; 2170 BP.
XX
AC   AAQ50870;
XX
DT   13-MAY-1994 (first entry)
XX
DE   p55 Tumour necrosis factor receptor coding sequence.
XX
KW   TNF; tumour necrosis factor; receptor; disease; autoimmunity;
KW   rheumatoid arthritis; graft rejection; graft vs host; septic shock;
KW   effector protein; ss.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   CDS   256..1623
FT   /*tag= a
FT   /product= p55 Tumour necrosis factor receptor.
XX
PN   EP568925-A.
XX
PD   10-NOV-1993.
XX
PF   29-APR-1993; 93EP-0106981
XX

us-09-525-998a-12.rng

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PR   03-MAY-1992   92H: 8103769.
XX
PA   (YEDA ) YEDA RES & DEV Co LTD.
XX
PI   Brakebusch C, Wallach D;
XX
DR   WPI; 1993-353057/45.
DR   P-PSDB: AAR42197.
XX
PT   Modulating activity of tumour necrosis factor receptor - using
PT   peptide(s), antibodies, etc. which interact with critical regions
PT   of receptor or effector protein, for controlling auto-immune
PT   disease, septic shock, etc.
XX
PS   Claim 1; Figure 1; 17pp; English
XX
CC   Modification of the tumour necrosis factor receptor by mutation or
CC   deletion modulates signal transduction and/or cleavage effected by
CC   the receptor. This modulation of activity can also be achieved
CC   using effector proteins which interact with the TNF receptor.
CC   Molecules which interact with the TNF receptor or the effector
CC   proteins can be used to treat or prevent diseases associated with
CC   TNF activity e.g. autoimmune disease; rheumatoid arthritis; graft
CC   rejection; graft vs. host disease or septic shock. They can also
CC   be used to treat overdoses of exogenous TNF.
XX
SQ   Sequence 2170 BP: 474 A; 657 C; 584 G; 455 T; 0 other;
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        Quality: 1108.50              Length:     211
        Ratio:   5.543                Gaps:       1
Percent Similarity: 94.787      Percent Identity: 93.839
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US-09-525-998A-12 x AAQ50870

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  17 uLeuLeuValGlyTyrTyrProSerGlyTyrValIleGly............... 29
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 406 GCTGTTGGTGGGTAATATACCCTCAGGGTTATTGGATGGTGGTGCCCTCACC 355

  30 ...........AspSerValCysProGlnGlyTyrTyrIle 39
                ||||||||||||||||||||||||||
 356 TAGGGACCACGAGAGAGACAATACGTGTCCCCAAGGGAAAATATATC 405

  40 HisProGlnAsnAsnSerIleCysCysThrLysCysHisLysGlyThr 56
     ||||||||||||||||||||||||||||||||||||||||||||||||
 406 CACCCCCAAAATAATTCGATTTGCTGCACACCCCAAGTGCCATAAAAGGAACCTA 455

  56 rLeuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArgGluC 73
     |||||||||||||||||||||||||||||||||||||||||||||||||
 456 CTTGTACAATGACTGTCCAGGTCCAGGTCAAGATACTGACTGCAGGGAAT 505

  73 ysGlnSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 89
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 506 GTCAGAGCGGCAGCTTCACCGCTTCAGAAAACCACCTCAGACACTGCCTC 555

  90 SerCysSerTyrCysArgTyrGluMetGlyGlnValGluIleSerSerCy 106
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 556 AGCTGCTCGTACTGCAGATACGAAATGGGCCAGGTGGAGATCTCTTC 605

 106 sThrValAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgH 123
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 606 CACAGTGGATCGAGATACCGTGTGCGGCTGTAGGAAGAACCAATACAGGCAT 655

 123 isTrpSerGluAsnLeuPheCysCysPheAsnCysSerLeuCysLeu 139
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 656 ATTATGGGAGTAAAACCTTTTGAGTGCTTCAATTGCAGCTTGTGCCTC 705

 140 AsnGlyThrValHisLeuSerCysCysGlnGluLysCysAsnThrValCysGln 156
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 706 AATGGCACTGTACACCTCTCTGCCAGGAGAAACAGAACACGGTGTGCAC 755

 156 rCysHisAlaGlyPhePheArgGluAsnGluCysValSerCysSerA 173
     |||||||||||||||||||||||||||||||||||||||||||||||
 756 CTGCCATGCAGGTTTCTTCAGAGAAAATGAGTGCGTCTCTGTAGTA 805

 173 SerCysValSerCysLysGlnCysProLysGluCysLeuProGlnIleGlu 189
     |||||||||||||||||||||||||||||||||||||||||||||||||||
 805 AGCTGCAAGAAAAGCCTGCAGCTGCACCAAGGTGTGCCTACCCCAATTGAG 855

 190 AsnValLysGlyThrGluAspSerGlyThrThr 200
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seq_documentation_block:
ID   AAQ12215 standard; DNA; 2176 BP.
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AC   AAQ12215;
XX
DT   12-SEP-1991 (first entry)
XX
DE   Type I TNF receptor.
XX
KW   Tumour Necrosis Factor; TNF; binding proteins; TBP-1; SS.
XX
OS   Homo sapiens.
XX
FH   Key                Location/Qualifiers
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FT   terminator         244..246
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FT   CDS                256..1620
FT                      /*tag= a
FT                      /product= "type I TNF receptor"
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FT   mat_peptide        319..1620
FT                      /*tag= c
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FT                      /note= "may be 2 codons shorter or a few codons
FT                      longer"
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FT   misc_feature       583..627
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FT                      /*tag= f
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FT   repeat_unit        485..504
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FT                      /number= 1
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FT                      /number= 2
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FT                     /*tag= m
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PN   EP433900-A.
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PD   26-JUN-1991.
XX
PF   13-DEC-1990;      90EP-0124133.
XX
PR   12-JUL-1990;      9011-0095064.
PR   13-DEC-1989;      8911-0092647.
XX
PA   (YEDA ) YEDA RES & DEV CO LTD.
XX
PI   Wallach D, Nophar Y, Kemper O, Engelmann H, Brakebusch C;
PI   Aderka D;
XX
DR   WPI: 1991-186774/26.
DR   P-PSDB: AAR12550
XX
PT   Recombinant tumour necrosis factor binding protein 1 prepd. by
PT   transfecting eukaryotic cells with vector contg. deoxyribonucleic
PI   acid encoding human type 1 TNF receptor or soluble domain
XX
PS   Disclosure; Fig 1(D); 38pp; English.
XX
CC   The Tumour Necrosis Factor Binding Protein 1 is the soluble form of
CC   type 1 TNF-receptor and constitutes a fragment of the cell surface
CC   form of this receptor, corresp. to its extracellular domain.
CC   There is no characteristic poly(A) addition signal near the 3' end
CC   of the cDNA.  The sequence ACTAAA (tag m) may serve as an
CC   alternative to this signal, but with low efficiency.
CC   See also AAQ12212-15.
XX
SQ   Sequence 2176 BP; 475 A, 644 C, 602 G, 455 T, 0 other;
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alignment_scores:
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         Quality: 1107.50           Length:    211
           Ratio: 5.565               Gaps:      1
Percent Similarity: 94.313   Percent Identity: 94.313
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alignment_block:
US-09-525-998A-12 x AAQ12215   ..

Align seg 1/1 to: AAQ12215 from: 1 to: 2176

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 17 uLeuLeuValGlyIleTyrProSerGlyValIleGly          29
    ||||||||||||||||||||||||||||||||||||||
306 GCTGTTGGTGGGAATATACCCTCAGGGGTTATTGGACTGGTGCCTCACC  355

 30 ...............AspSerValCysProGluGlyLysTyrIle  39
                   ||||||||||||||||||||||||||||||
356 TAGGGACAGGAACAGCAAGAGAAAGTGCGTCGTGCCAAGGAAAAATATC  405

 40 HisProGlnAsnAsnSerIleCysCysThrLysCysHisLysGlyThrTy  56
    |||||||||||||||||||||||||||||||  ||||||||||||||||
406 CACCCTCAAATAATTGGAATTGCAGTACCAAGTGCCACAAAGGAACCTA  455

 56 rLeuTyrAsnAspCysProGlyProGlyGlnAspThrAspCysArgGluC  73
    ||||||||||||||||||||||||||||||||||||||||||||||||
456 CTTGTACAATGACTGTCCAGGCCCAGGGCAGGATACTGACTGCAGGGAGT  505

 73 ysGluSerGlySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu  89
    ||||||||||||||||||||||||||||||||||||||||||||||||||
506 GTGAGAGCGGCTCCTTCACCGCTTCAGAAAACCACCTCAGACACTCCCTC  555

 90 SerCysSerLysCysArgLysGluMetGlyGlnValGluIleSerSerCy  106
    ||||||||||||||||||||||||||||||||||||||||||||||||||
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Right column:
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556 AGTGCTCCAAATGCCGAAAGGAAATGGGCCAGGTGGAGATCTCTTCTTG  605

106 sThrValAspArgAspThrValCysGlyCysArgLysAsnGlnTyrArgH  123
    ||||||||||||||||||||||||||||||||||||||||||||||||||
606 CACAGGGACAGGGACACAGTGTGTGGCTGCAGAAAGAACCAGTACCGGC  655

123 isTyrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu  139
    ||||||||||||||||||||||||||||||||||||||||||||||||||
656 ATTATTGGAGTGAAAACCTTTTCCAGTGCTTCAATTGCAGCCTCTGCCTC  705

140 AsnGlyThrValHisLeuSerCysGlnGluLysGlnAsnThrValCysTh  156
    ||||||||||||||||||||||||||||||||||||||||||||||||||
706 AATGGGACCGTGCACCTCTCCTGCCAGGAGAAACAGAACACCGTGTGCAC  755

156 rCysHisAlaGlyPhePheLeuArgGluAsnGluCysValSerCysSerA  173
    ||||||||||||||||||||||||||||||||||||||||||||||||||
756 CTGCCATGCAGGTTTCTTTCTAAGAGAAAACGAGTGTGTCTCCTGTAGTA  805

173 snCysLysLysSerLeuGluCysThrLysLeuProGlnIleGlu  189
    ||||||||||||||||||||||||||||||||||||||||
806 ACTGTAAGAAAAGCCTGGAGTGCACGAAGTTGCCTCAGATTGAG  855

190 AsnValLysGlyThrGluAspSerGlyThrThr  200
    ||||||||||||||||||||||||||||||
856 AATGTTAAGGCACTGAGGACTCAGGCACCACA  888
```

us-09-525-998a-12.rng